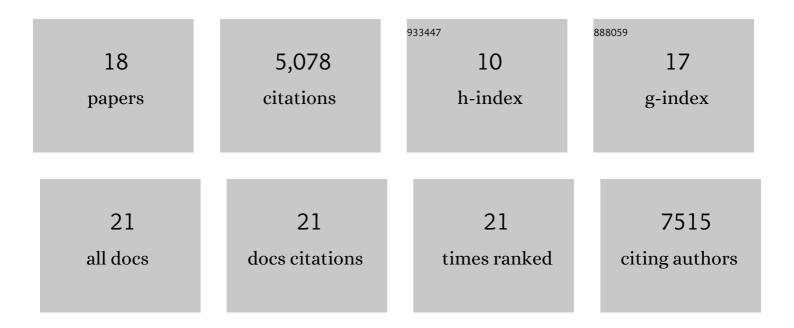
## Susan Bassham

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5893497/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Single-cell Iso-Sequencing enables rapid genome annotation for scRNAseq analysis. Genetics, 2022, 220,	2.9	10
2	Leafy and weedy seadragon genomes connect genic and repetitive DNA features to the extravagant biology of syngnathid fishes. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	8
3	Genomeâ€wide single nucleotide polymorphism markers reveal population structure and dispersal direction of an expanding nuisance algal bloom species. Molecular Ecology, 2021, 30, 912-925.	3.9	13
4	Chromonomer: A Tool Set for Repairing and Enhancing Assembled Genomes Through Integration of Genetic Maps and Conserved Synteny. G3: Genes, Genomes, Genetics, 2020, 10, 4115-4128.	1.8	44
5	Highly Reproducible 16S Sequencing Facilitates Measurement of Host Genetic Influences on the Stickleback Gut Microbiome. MSystems, 2019, 4, .	3.8	8
6	Repeated Selection of Alternatively Adapted Haplotypes Creates Sweeping Genomic Remodeling in Stickleback. Genetics, 2018, 209, 921-939.	2.9	64
7	Ancient three-spined stickleback (Gasterosteus aculeatus) mtDNA lineages are not associated with phenotypic or nuclear genetic variation. Biological Journal of the Linnean Society, 2017, 122, 579-588.	1.6	4
8	Developmental timing differences underlie armor loss across threespine stickleback populations. Evolution & Development, 2017, 19, 231-243.	2.0	7
9	Host Genotype and Microbiota Contribute Asymmetrically to Transcriptional Variation in the Threespine Stickleback Gut. Genome Biology and Evolution, 2017, 9, 504-520.	2.5	40
10	Remembering James Alan Bassham (1922–2012). Photosynthesis Research, 2016, 128, 3-13.	2.9	10
11	Response to May and Delany: We Never Said Wright was Wrong. Journal of Heredity, 2015, 106, esv072.	2.4	Ο
12	Effects of Crossovers Between Homeologs on Inheritance and Population Genomics in Polyploid-Derived Salmonid Fishes. Journal of Heredity, 2015, 106, 217-227.	2.4	97
13	Stacks: an analysis tool set for population genomics. Molecular Ecology, 2013, 22, 3124-3140.	3.9	3,077
14	The population structure and recent colonization history of <scp>O</scp> regon threespine stickleback determined using restrictionâ€site associated <scp>DNA</scp> â€sequencing. Molecular Ecology, 2013, 22, 2864-2883.	3.9	119
15	Local De Novo Assembly of RAD Paired-End Contigs Using Short Sequencing Reads. PLoS ONE, 2011, 6, e18561.	2.5	187
16	Population Genomics of Parallel Adaptation in Threespine Stickleback using Sequenced RAD Tags. PLoS Genetics, 2010, 6, e1000862.	3.5	1,219
17	Development of the central nervous system in the larvacean Oikopleura dioica and the evolution of the chordate brain. Developmental Biology, 2005, 285, 298-315.	2.0	107
18	Brachyury (T) Expression in Embryos of a Larvacean Urochordate, Oikopleura dioica, and the Ancestral Role of T. Developmental Biology, 2000, 220, 322-332.	2.0	63